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RAW SEQUENCE LISTING   DATE: 04/11/2002
PATENT APPLICATION: US/10/044,622   TIME: 09:14:18

Input Set : N:\Crf3\RULE60\10044622.raw
Output Set: N:\CRF3\04112002\J044622.raw

ENTERED

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      SEQUENCE LISTING
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Bandman, Olga
 6                     ·Goli, Surya K.
 7                      Murry, Lynn E.
 9     (ii) TITLE OF INVENTION: NOVEL ENDOTHELIAL GROWTH
10                             FACTOR
12    (iii) NUMBER OF SEQUENCES: 3
14     (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
16          (B) STREET: 3174 Porter Drive
17          (C) CITY: Palo Alto
18          (D) STATE: CA
19          (E) COUNTRY: USA
20          (F) ZIP: 94304
22      (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Diskette
24          (B) COMPUTER: IBM Compatible
25          (C) OPERATING SYSTEM: DOS
26          (D) SOFTWARE: FastSEQ for Windows Version 2.0
28     (vi) CURRENT APPLICATION DATA:
29          (A) APPLICATION NUMBER: US/10/044,622        C-->
30          (B) FILING DATE: 09-Jan-2002                 C-->
31          (C) CLASSIFICATION:
33    (vii) PRIOR APPLICATION DATA:
34          (A) APPLICATION NUMBER: 08/788,812
35          (B) FILING DATE:
37   (viii) ATTORNEY/AGENT INFORMATION:
38          (A) NAME: Billings, Lucy J.
39          (B) REGISTRATION NUMBER: 36,749
40          (C) REFERENCE/DOCKET NUMBER: PF-0185 US
42     (ix) TELECOMMUNICATION INFORMATION:
43          (A) TELEPHONE: 415-855-0555
44          (B) TELEFAX: 415-845-4166
46 (2) INFORMATION FOR SEQ ID NO: 1:
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 280 amino acids
50          (B) TYPE: amino acid
51          (C) STRANDEDNESS: single
52          (D) TOPOLOGY: linear
54    (vii) IMMEDIATE SOURCE:
55          (A) LIBRARY: LUNGAST01
56          (B) CLONE: 873352
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```
58      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
60  Met Tyr Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val
61  1               5               10              15
62  Gln Leu Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser
63              20              25              30
64  Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
65          35              40              45
66  Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
67      50              55              60
68  Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
69  65              70              75              80
70  Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
71              85              90              95
72  Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
73              100             105             110
74  Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
75          115             120             125
76  Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
77      130             135             140
78  Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
79  145             150             155             160
80  Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
81              165             170             175
82  Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
83              180             185             190
84  Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
85          195             200             205
86  Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
87      210             215             220
88  Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
89  225             230             235             240
90  Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
91              245             250             255
92  Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
93          260             265             270
94  Cys Lys Thr Pro Cys Pro Lys Ile
95          275             280
97 (2) INFORMATION FOR SEQ ID NO: 2:
99      (i) SEQUENCE CHARACTERISTICS:
100         (A) LENGTH: 1337 base pairs
101         (B) TYPE: nucleic acid
102         (C) STRANDEDNESS: single
103         (D) TOPOLOGY: linear
105     (vii) IMMEDIATE SOURCE:
106         (A) LIBRARY: LUNGAST01
107         (B) CLONE: 873352
109     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
111  CTGTAATAGG AGCAGTATAG GGAAACCTGG TACCCTGCAG GTACTGGTCC GGAGTTCCTG    60
112  GGTCGACCCA CGCGTCCGGC TTTCTGTAGC TGTAACATTG GTGGCCACAC ACCTCCTTAC   120
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113  AAAGCAACTA GAACCTGCGG CATACATTGG AGAGATTTTT TTAATTTTCT GGACATGAAG  180
114  TAAATTTAGA GTGCTTTCTA ATTTCAGGTA GAAGACATGT CCACCTTCTG ATTATTTTTG  240
115  GAGAACATTT TGATTTTTTT CATCTCTCTC TCCCCACCCC TAAGATTGTG CAAAAAAAGC  300
116  GTACCTTGCC TAATTGAAAT AATTTCATTG GATTTTGATC AGAACTGATT ATTTGGTTTT  360
117  CTGTGTGAAG TTTTGAGGTT TCAAACTTTC CTTCTGGAGA ATGCCTTTTG AAACAATTTT  420
118  CTCTAGCTGC CTGATGTCAA CTGCTTAGTA ATCAGTGGAT ATTGAAATAT TCAAAATGTA  480
119  CAGAGAGTGG GTAGTGGTGA ATGTTTTCAT GATGTTGTAC GTCCAGCTGG TGCAGGGCTC  540
120  CAGTAATGAA CATGGACCAG TGAAGCGATC ATCTCAGTCC ACATTGGAAC GATCTGAACA  600
121  GCAGATCAGG GCTGCTTCTA GTTTGGAGGA ACTACTTCGA ATTACTCACT CTGAGGACTG  660
122  GAAGCTGTGG AGATGCAGGC TGAGGCTCAA AAGTTTTACC AGTATGGACT CTCGCTCAGC  720
123  ATCCCATCGG TCCACTAGGT TTGCGGCAAC TTTCTATGAC ATTGAAACAC TAAAAGTTAT  780
124  AGATGAAGAA TGGCAAAGAA CTCAGTGCAG CCCTAGAGAA ACGTGCGTGG AGGTGGCCAG  840
125  TGAGCTGGGG AAGAGTACCA ACACATTCTT CAAGCCCCCT TGTGTGAACG TGTTCCGATG  900
126  TGGTGGCTGT TGCAATGAAG AGAGCCTTAT CTGTATGAAC ACCAGCACCT CGTACATTTC  960
127  CAAACAGCTC TTTGAGATAT CAGTGCCTTT GACATCAGTA CCTGAATTAG TGCCTGTTAA  1020
128  AGTTGCCAAT CATACAGGTT GTAAGTGCTT GCCAACAGCC CCCCGCCATC CATACTCAAT  1080
129  TATCAGAAGA TCCATCCAGA TCCCTGAAGA AGATCGCTGT TCCCATTCCA AGAAACTCTG  1140
130  TCCTATTGAC ATGCTATGGG ATAGCAACAA ATGTAAATGT GTTTTGCAGG AGGAAAATCC  1200
131  ACTTGCTGGA ACAGAAGACC ACTCTCATCT CCAGGAACCA GCTCTCTGTG GGCCACACAT  1260
132  GATGTTTGAC GAAGATCGTT GCGAGTGTGT CTGTAAAACA CCATGTCCCA AGATCTAATC  1320
133  CAGCACCCCA AAAAATG                                                 1337
```

135 (2) INFORMATION FOR SEQ ID NO: 3:
137   (i) SEQUENCE CHARACTERISTICS:
138   (A) LENGTH: 419 amino acids
139   (B) TYPE: amino acid
140   (C) STRANDEDNESS: single
141   (D) TOPOLOGY: linear
143   (vii) IMMEDIATE SOURCE:
144   (A) LIBRARY: GenBank
145   (B) CLONE: 1150989
147   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
149  Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
150  1               5                   10                  15
151  Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
152                20                  25                  30
153  Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
154                35                  40                  45
155  Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
156      50                  55                  60
157  Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
158  65                  70                  75                  80
159  Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
160                  85                  90                  95
161  Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
162                100                 105                 110
163  His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
164                115                 120                 125
165  Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
166                130                 135                 140
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167  Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
168  145             150             155             160
169  Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
170              165             170             175
171  Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
172          180             185             190
173  Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
174          195             200             205
175  Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
176      210             215             220
177  Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
178  225             230             235             240
179  Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
180              245             250             255
181  Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
182          260             265             270
183  Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
184          275             280             285
185  Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
186      290             295             300
187  Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
188  305             310             315             320
189  Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
190              325             330             335
191  Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
192          340             345             350
193  Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
194          355             360             365
195  Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
196      370             375             380
197  Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
198  385             390             395             400
199  Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
200              405             410             415
201  Gln Met Ser
```

VERIFICATION SUMMARY   DATE: 04/11/2002
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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]